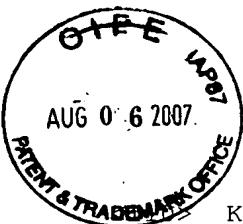


SEQUENCE LISTING



Kesseler, Maria
Zelinski, Thomas
Hauer, Bernhard

<120> L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS
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<150> PCT/EP2003/013367
<151> 2003-11-27
<150> DE 102 56 381.0
<151> 2002-12-02
<160> 24
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<220>
 <221> promoter
 <222> (1)..(287)
 <223> rhaBAD promoter fragment containing rhaS and rhaR binding sites

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 taaattttcg acggaaaacc acgtaaaaaaa cgtcgatattt tcaagataca gcgtgaattt 120
 tcaggaaatg cggtgcgtatc cacaatccca caattcagca aattgtgaac atcatcacgt 180
 tcacatccctt cttgggttgcata atggcccatt ttcctgtcgt taacgagaag gtcgcgtt 240
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<210> 3
 <211> 125
 <212> DNA
 <213> Escherichia coli

<220>

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<221> promoter
<222> (1)..(125)
<223> rhaBAD promoter fragment containing RhaS binding site

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acgagaaggc cgcgaaattca ggcgcctttt agactggtcg taatgaaattt cagcaggatc 120
acatt                                         125

<210> 4
<211> 123
<212> DNA
<213> Escherichia coli

<220>
<221> promoter
<222> (1)..(123)
<223> rhaBAD promoter fragment containing RhaS binding site

<400> 4
atcaccacaa tttagccaaat tgtgaacatc atcacgttca tctttccctg gttgccaatg 60
gcccattttc ctgtcagtaa cgagaaggc gcgaatttgc ggcgcctttt gactggtcgt 120
aat                                         123

<210> 5
<211> 51
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)..(51)
<223> palindromic RhaS binding site of rhaBAD promoter

<400> 5
atcttccct ggttgccaat ggcccatttt cctgtcagta acgagaaggc 51
                                         51

<210> 6
<211> 1071
<212> DNA
<213> Alcaligenes faecalis

<220>
<221> CDS
<222> (1)..(1068)
<223> coding for nitrilase

<400> 6
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Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
   1           5           10          15
ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct 96
Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
   20          25          30
cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc 144
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
   35          40          45
tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg 192
                                         
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Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp		
50 55 60		
tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac	240	
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp		
65 70 75 80		
agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att	288	
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile		
85 90 95		
ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg	336	
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu		
100 105 110		
ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc	384	
Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg		
115 120 125		
aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat	432	
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr		
130 135 140		
gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct	480	
Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala		
145 150 155 160		
cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac	528	
Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr		
165 170 175		
tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta	576	
Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu		
180 185 190		
tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc	624	
Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala		
195 200 205		
tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc	672	
Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser		
210 215 220		
agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac	720	
Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His		
225 230 235 240		
aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg	768	
Asn Ala Pro Leu Leu Lys Val Gly Gly Ser Ser Met Ile Phe Ala		
245 250 255		
ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc	816	
Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly		
260 265 270		
ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg	864	
Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala		
275 280 285		
atc aat gac ccc gta ggc cac tat tcc aaa ccc gag gcc acc cgt ctg	912	
Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu		
290 295 300		
gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa	960	
Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys		
305 310 315 320		
agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att	1008	
Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile		
325 330 335		
gcc tca gtc gct atc agc cat cca cag gac tcg gac aca ctg cta gtg	1056	
Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val		
340 345 350		
caa gag ccg tct tga	1071	
Gln Glu Pro Ser		
355		

<210> 7
<211> 356
<212> PRT
<213> Alcaligenes faecalis

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Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
35 40 45
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
50 55 60
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
65 70 75 80
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
85 90 95
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
100 105 110
Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
115 120 125
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
130 135 140
Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
145 150 155 160
Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
165 170 175
Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
180 185 190
Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
195 200 205
Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
210 215 220
Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
225 230 235 240
Asn Ala Pro Leu Leu Lys Val Gly Gly Ser Ser Met Ile Phe Ala
245 250 255
Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
260 265 270
Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
275 280 285
Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
290 295 300
Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
305 310 315 320
Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
325 330 335
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340 345 350
Gln Glu Pro Ser
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<210> 8
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<213> Escherichia coli

<220>
<221> CDS

<222> (1)..(1257)

<223> coding for rhaA (L-rhamnose isomerase)

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gct gct gtg ggg att gat gtc gag gag gct cgc cca ctt gat cgt	96
Ala Ala Val Gly Ile Asp Val Glu Ala Leu Arg Gln Leu Asp Arg	
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tta ccc gtt tca atg cac tgc tgg cag ggc gat gat gtt tcc ggt ttt	144
Leu Pro Val Ser Met His Cys Trp Gln Gly Asp Asp Val Ser Gly Phe	
35 40 45	
gaa aac ccg gaa ggt tcg acc ggg ggg att cag gcc aca ggc aat	192
Glu Asn Pro Glu Gly Ser Leu Thr Gly Gly Ile Gln Ala Thr Gly Asn	
50 55 60	
tat ccg ggc aaa gct cgt aat gcc agt gag cta cgt gcc gat ctg gaa	240
Tyr Pro Gly Lys Ala Arg Asn Ala Ser Glu Leu Arg Ala Asp Leu Glu	
65 70 75 80	
cag gct atg cgg ctg att ccg ggg ccg aaa ccg ctt aat tta cat gcc	288
Gln Ala Met Arg Leu Ile Pro Gly Pro Lys Arg Leu Asn Leu His Ala	
85 90 95.	
atc tat ctg gaa tca gat acg cca gtc tcg cgc gac cag atc aaa cca	336
Ile Tyr Leu Glu Ser Asp Thr Pro Val Ser Arg Asp Gln Ile Lys Pro	
100 105 110	
gag cac ttc aaa aac tgg gtt gaa tgg gct aaa gcc aat cag ctc ggt	384
Glu His Phe Lys Asn Trp Val Glu Trp Ala Lys Ala Asn Gln Leu Gly	
115 120 125	
ctg gat ttt aac ccc tcc tgc ttt tcg cat ccg cta agc gcc gat ggc	432
Leu Asp Phe Asn Pro Ser Cys Phe Ser His Pro Leu Ser Ala Asp Gly	
130 135 140	
ttt acg ctt tcc cat gcc gac gac att cgc cag ttc tgg att gat	480
Phe Thr Leu Ser His Ala Asp Asp Ser Ile Arg Gln Phe Trp Ile Asp	
145 150 155 160	
cac tgc aaa gcc agc cgt cgc gtt tcg gcc tat ttt ggc gag caa ctc	528
His Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu	
165 170 175	
ggc aca cca tcg gtg atg aac atc tgg atc ccg gat ggt atg aaa gat	576
Gly Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp	
180 185 190	
atc acc gtt gac cgt ctc gcc ccg cgt cag cgt ctg ctg gca gca ctg	624
Ile Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu	
195 200 205	
gat gag gtg atc agc gag aag cta aac cct gct cac cat atc gac gcc	672
Asp Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala	
210 215 220	
gtt gag agc aaa ttg ttt ggc att ggc gca gag agc tac acg gtt ggc	720
Val Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly	
225 230 235 240	
tcc aat gag ttt tac atg ggg tat gcc acc agc cgc cag act gct ctg	768
Ser Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu	
245 250 255	
tgc ctg gac gcc ggg cac ttc cac ccg act gaa gtg att tcc gac aag	816
Cys Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys	
260 265 270	
att tcc gcc gcc atg ctg tat gtg ccg cag ttg ctg ctg cac gtc agc	864
Ile Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu His Val Ser	
275 280 285	
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Arg Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu	
290 295 300	

acc cag gca att gcc agt gag att gtg cgt cac gat ctg ttt gac cg	960
Thr Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg	
305 310 315 320	
gtg cat atc ggc ctt gac ttc ttc gat gcc tct atc aac cgc att gcc	1008
Val His Ile Gly Leu Asp Phe Asp Ala Ser Ile Asn Arg Ile Ala	
325 330 335	
gcu tgg gtc att ggt aca cgc aat atg aaa aaa gcc ctg ctg cgt g	1056
Ala Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala	
340 345 350	
ttg ctg gaa cct acc gct gac gtg cgc aag ctg gaa gcg ggc gat	1104
Leu Leu Glu Pro Thr Ala Asp Val Arg Lys Leu Glu Ala Ala Gly Asp	
355 360 365	
tac act gcg cgt ctg gca ctg ctg gaa gag cag aaa tcg ttg ccg tgg	1152
Tyr Thr Ala Arg Leu Ala Leu Leu Glu Glu Gln Lys Ser Leu Pro Trp	
370 375 380	
cag gcg gtc tgg gaa atg tat tgc caa cgt cac gat acg cca gca ggt	1200
Gln Ala Val Trp Glu Met Tyr Cys Gln Arg His Asp Thr Pro Ala Gly	
385 390 395 400	
agc gaa tgg ctg gag agc gtg cgg gct tat gag aaa gaa att ttg agt	1248
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405 410 415	
cgc cgc ggg taa	1260
Arg Arg Gly	

<210> 9
<211> 419
<212> PRT
<213> Escherichia coli

<400> 9	
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35 40 45	
Glu Asn Pro Glu Gly Ser Leu Thr Gly Gly Ile Gln Ala Thr Gly Asn	
50 55 60	
Tyr Pro Gly Lys Ala Arg Asn Ala Ser Glu Leu Arg Ala Asp Leu Glu	
65 70 75 80	
Gln Ala Met Arg Leu Ile Pro Gly Pro Lys Arg Leu Asn Leu His Ala	
85 90 95	
Ile Tyr Leu Glu Ser Asp Thr Pro Val Ser Arg Asp Gln Ile Lys Pro	
100 105 110	
Glu His Phe Lys Asn Trp Val Glu Trp Ala Lys Ala Asn Gln Leu Gly	
115 120 125	
Leu Asp Phe Asn Pro Ser Cys Phe Ser His Pro Leu Ser Ala Asp Gly	
130 135 140	
Phe Thr Leu Ser His Ala Asp Asp Ser Ile Arg Gln Phe Trp Ile Asp	
145 150 155 160	
His Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu	
165 170 175	
Gly Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp	
180 185 190	
Ile Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu	
195 200 205	
Asp Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala	
210 215 220	
Val Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly	
225 230 235 240	

Ser Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu
 245 250 255
 Cys Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys
 260 265 270
 Ile Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu Leu His Val Ser
 275 280 285
 Arg Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu
 290 295 300
 Thr Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg
 305 310 315 320
 Val His Ile Gly Leu Asp Phe Phe Asp Ala Ser Ile Asn Arg Ile Ala
 325 330 335
 Ala Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala
 340 345 350
 Leu Leu Glu Pro Thr Ala Asp Val Arg Lys Leu Glu Ala Ala Gly Asp
 355 360 365
 Tyr Thr Ala Arg Leu Ala Leu Leu Glu Glu Gln Lys Ser Leu Pro Trp
 370 375 380
 Gln Ala Val Trp Glu Met Tyr Cys Gln Arg His Asp Thr Pro Ala Gly
 385 390 395 400
 Ser Glu Trp Leu Glu Ser Val Arg Ala Tyr Glu Lys Glu Ile Leu Ser
 405 410 415
 Arg Arg Gly

<210> 10
 <211> 1470
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1467)
 <223> coding for rhaB (rhamnolukinase)

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 cgc gtg atg ctg gcg cgt tac gag cgt gaa tgc cgc agc ctg acg ctg 96
 Arg Val Met Leu Ala Arg Tyr Glu Arg Glu Cys Arg Ser Leu Thr Leu
 20 25 30
 cgc gaa atc cat cgt ttt aac aat ggg ctg cat agt cag aac ggc tat 144
 Arg Glu Ile His Arg Phe Asn Asn Gly Leu His Ser Gln Asn Gly Tyr
 35 40 45
 gtc acc tgg gat gtg gat agc ctt gaa agt gcc att cgc ctt gga tta 192
 Val Thr Trp Asp Val Asp Ser Leu Glu Ser Ala Ile Arg Leu Gly Leu
 50 55 60
 aac aag gtg tgc gag gaa ggg att cgt atc gat agc att ggg att gat 240
 Asn Lys Val Cys Glu Gly Ile Arg Ile Asp Ser Ile Gly Ile Asp
 65 70 75 80
 acc tgg ggc gtg gac ttt gtg ctg ctc gac caa cag ggt cag cgt gtg 288
 Thr Trp Gly Val Asp Phe Val Leu Leu Asp Gln Gln Gly Gln Arg Val
 85 90 95
 ggc ctg ccc gtt gct tat cgc gat agc cgc acc aat ggc cta atg gcg 336
 Gly Leu Pro Val Ala Tyr Arg Asp Ser Arg Thr Asn Gly Leu Met Ala
 100 105 110
 cag gca caa caa ctt ggc aaa cgc gat att tat caa cgt agc ggc 384
 Gln Ala Gln Gln Leu Gly Lys Arg Asp Ile Tyr Gln Arg Ser Gly
 115 120 125
 atc cag ttt ctg ccc ttc aat acg ctt tat cag ttg cgt gcg ctg acg 432

Ile Gln Phe Leu Pro Phe Asn Thr Leu Tyr Gln Leu Arg Ala Leu Thr			
130	135	140	
gag caa caa cct gaa ctt att cca cac att gct cac gct ctg ctg atg			480
Glu Gln Gln Pro Glu Leu Ile Pro His Ile Ala His Ala Leu Leu Met			
145	150	155	160
ccg gat tac ttc agt tat cgc ctg acc ggc aag atg aac tgg gaa tat			528
Pro Asp Tyr Phe Ser Tyr Arg Leu Thr Gly Lys Met Asn Trp Glu Tyr			
165	170	175	
acc aac gcc acg acc acg caa ctg gtc aat atc aat agc gac gac tgg			576
Thr Asn Ala Thr Thr Gln Leu Val Asn Ile Asn Ser Asp Asp Trp			
180	185	190	
gac gag tcg cta ctg gcg tgg agc ggg gcc aac aaa gcc tgg ttt ggt			624
Asp Glu Ser Leu Leu Ala Trp Ser Gly Ala Asn Lys Ala Trp Phe Gly			
195	200	205	
cgc ccg acg cat ccg ggt aat gtc ata ggt cac tgg att tgc ccg cag			672
Arg Pro Thr His Pro Gly Asn Val Ile Gly His Trp Ile Cys Pro Gln			
210	215	220	
ggt aat gag att cca gtg gtc gcc gtt gcc agc cat gat acc gcc agc			720
Gly Asn Glu Ile Pro Val Val Ala Val Ala Ser His Asp Thr Ala Ser			
225	230	235	240
gcg gtt atc gcc tcg ccg tta aac ggc tca cgt gct gct tat ctc tct			768
Ala Val Ile Ala Ser Pro Leu Asn Gly Ser Arg Ala Ala Tyr Leu Ser			
245	250	255	
tct ggc acc tgg tca ttg atg ggc ttc gaa agc cag acg cca ttt acc			816
Ser Gly Thr Trp Ser Leu Met Gly Phe Glu Ser Gln Thr Pro Phe Thr			
260	265	270	
aat gac acg gca ctg gca gcc aac atc acc aat gaa ggc ggg gcg gaa			864
Asn Asp Thr Ala Leu Ala Ala Asn Ile Thr Asn Glu Gly Gly Ala Glu			
275	280	285	
ggt cgc tat cgg gtg ctg aaa aat att atg ggc tta tgg ctg ctt cag			912
Gly Arg Tyr Arg Val Leu Lys Asn Ile Met Gly Leu Trp Leu Leu Gln			
290	295	300	
cga gtg ctt cag gag cag caa atc aac gat ctt ccg gcg ctt atc tcc			960
Arg Val Leu Gln Glu Gln Ile Asn Asp Leu Pro Ala Leu Ile Ser			
305	310	315	320
gcg aca cag gca ctt ccg gct tgc cgc ttc att atc aat ccc aat gac			1008
Ala Thr Gln Ala Leu Pro Ala Cys Arg Phe Ile Ile Asn Pro Asn Asp			
325	330	335	
gat cgc ttt att aat cct gag acg atg tgc agc gaa att cag gct gcg			1056
Asp Arg Phe Ile Asn Pro Glu Thr Met Cys Ser Glu Ile Gln Ala Ala			
340	345	350	
tgt cgg gaa acg gcg caa ccg atc ccg gaa agt gat gct gaa ctg gcg			1104
Cys Arg Glu Thr Ala Gln Pro Ile Pro Glu Ser Asp Ala Glu Leu Ala			
355	360	365	
cgc tgc att ttc gac agt ctg gcg ctg ctg tat gcc gat gtg ttg cat			1152
Arg Cys Ile Phe Asp Ser Leu Ala Leu Leu Tyr Ala Asp Val Leu His			
370	375	380	
gag ctg gcg cag ctg cgc ggt gaa gat ttc tcg caa ctg cat att gtc			1200
Glu Leu Ala Gln Leu Arg Gly Glu Asp Phe Ser Gln Leu His Ile Val			
385	390	395	400
ggc gga ggc tgc cag aac acg ctg ctc aac cag cta tgc gcc gat gcc			1248
Gly Gly Cys Gln Asn Thr Leu Leu Asn Gln Leu Cys Ala Asp Ala			
405	410	415	
tgc ggt att cgg gtg atc gcc ggg cct gtt gaa gcc tcg acg ctc ggc			1296
Cys Gly Ile Arg Val Ile Ala Gly Pro Val Glu Ala Ser Thr Leu Gly			
420	425	430	
aat atc ggc atc cag tta atg acg ctg gat gaa ctc aac aat gtg gat			1344
Asn Ile Gly Ile Gln Leu Met Thr Leu Asp Glu Leu Asn Asn Val Asp			
435	440	445	
gat ttc cgt cag gtc gtc agc acc acc gcg aat ctg acc acc acc ttt acc			1392
Asp Phe Arg Gln Val Val Ser Thr Thr Ala Asn Leu Thr Phe Thr			

450	455	460	
cct aat cct gac agt gaa att gcc cac tat gtg gcg cag att cac tct			1440
Pro Asn Pro Asp Ser Glu Ile Ala His Tyr Val Ala Gln Ile His Ser			
465	470	475	480
aca cga cag aca aag gag ctt tgc gca tga			
Thr Arg Gln Thr Lys Glu Leu Cys Ala			1470
	485		

<210> 11
<211> 489
<212> PRT
<213> Escherichia coli

<400> 11			
Met Thr Phe Arg Asn Cys Val Ala Val Asp Leu Gly Ala Ser Ser Gly			
1	5	10	15
Arg Val Met Leu Ala Arg Tyr Glu Arg Glu Cys Arg Ser Leu Thr Leu			
20	25	30	
Arg Glu Ile His Arg Phe Asn Asn Gly Leu His Ser Gln Asn Gly Tyr			
35	40	45	
Val Thr Trp Asp Val Asp Ser Leu Glu Ser Ala Ile Arg Leu Gly Leu			
50	55	60	
Asn Lys Val Cys Glu Glu Gly Ile Arg Ile Asp Ser Ile Gly Ile Asp			
65	70	75	80
Thr Trp Gly Val Asp Phe Val Leu Leu Asp Gln Gln Gly Gln Arg Val			
85	90	95	
Gly Leu Pro Val Ala Tyr Arg Asp Ser Arg Thr Asn Gly Leu Met Ala			
100	105	110	
Gln Ala Gln Gln Gln Leu Gly Lys Arg Asp Ile Tyr Gln Arg Ser Gly			
115	120	125	
Ile Gln Phe Leu Pro Phe Asn Thr Leu Tyr Gln Leu Arg Ala Leu Thr			
130	135	140	
Glu Gln Gln Pro Glu Leu Ile Pro His Ile Ala His Ala Leu Leu Met			
145	150	155	160
Pro Asp Tyr Phe Ser Tyr Arg Leu Thr Gly Lys Met Asn Trp Glu Tyr			
165	170	175	
Thr Asn Ala Thr Thr Gln Leu Val Asn Ile Asn Ser Asp Asp Trp			
180	185	190	
Asp Glu Ser Leu Leu Ala Trp Ser Gly Ala Asn Lys Ala Trp Phe Gly			
195	200	205	
Arg Pro Thr His Pro Gly Asn Val Ile Gly His Trp Ile Cys Pro Gln			
210	215	220	
Gly Asn Glu Ile Pro Val Val Ala Val Ala Ser His Asp Thr Ala Ser			
225	230	235	240
Ala Val Ile Ala Ser Pro Leu Asn Gly Ser Arg Ala Ala Tyr Leu Ser			
245	250	255	
Ser Gly Thr Trp Ser Leu Met Gly Phe Glu Ser Gln Thr Pro Phe Thr			
260	265	270	
Asn Asp Thr Ala Leu Ala Asn Ile Thr Asn Glu Gly Ala Glu			
275	280	285	
Gly Arg Tyr Arg Val Leu Lys Asn Ile Met Gly Leu Trp Leu Leu Gln			
290	295	300	
Arg Val Leu Gln Glu Gln Ile Asn Asp Leu Pro Ala Leu Ile Ser			
305	310	315	320
Ala Thr Gln Ala Leu Pro Ala Cys Arg Phe Ile Ile Asn Pro Asn Asp			
325	330	335	
Asp Arg Phe Ile Asn Pro Glu Thr Met Cys Ser Glu Ile Gln Ala Ala			
340	345	350	
Cys Arg Glu Thr Ala Gln Pro Ile Pro Glu Ser Asp Ala Glu Leu Ala			
355	360	365	

Arg Cys Ile Phe Asp Ser Leu Ala Leu Leu Tyr Ala Asp Val Leu His
 370 375 380
 Glu Leu Ala Gln Leu Arg Gly Glu Asp Phe Ser Gln Leu His Ile Val
 385 390 395 400
 Gly Gly Cys Gln Asn Thr Leu Leu Asn Gln Leu Cys Ala Asp Ala
 405 410 415
 Cys Gly Ile Arg Val Ile Ala Gly Pro Val Glu Ala Ser Thr Leu Gly
 420 425 430
 Asn Ile Gly Ile Gln Leu Met Thr Leu Asp Glu Leu Asn Asn Val Asp
 435 440 445
 Asp Phe Arg Gln Val Val Ser Thr Thr Ala Asn Leu Thr Thr Phe Thr
 450 455 460
 Pro Asn Pro Asp Ser Glu Ile Ala His Tyr Val Ala Gln Ile His Ser
 465 470 475 480
 Thr Arg Gln Thr Lys Glu Leu Cys Ala
 485

<210> 12
 <211> 825
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(822)
 <223> coding for rhaD (rhamnulose-phosphate aldolase)

<400> 12

atg caa aac att act cag tcc tgg ttt gtc cag gga atg atc aaa gcc	48
Met Gln Asn Ile Thr Gln Ser Trp Phe Val Gln Gly Met Ile Lys Ala	
1 5 10 15	
acc acc gac gcc tgg ctg aaa ggc tgg gat gag cgc aac ggc ggc aac	96
Thr Thr Asp Ala Trp Leu Lys Gly Trp Asp Glu Arg Asn Gly Asn	
20 25 30	
ctg acg cta cgc ctg gat gac gcc gat atc gca cca tat cac gac aat	144
Leu Thr Leu Arg Leu Asp Asp Ala Asp Ile Ala Pro Tyr His Asp Asn	
35 40 45	
ttc cac caa caa ccg cgc tat atc ccg ctc agc cag ccc atg cct tta	192
Phe His Gln Gln Pro Arg Tyr Ile Pro Leu Ser Gln Pro Met Pro Leu	
50 55 60	
ctg gca aat aca ccg ttt att gtc acc ggc tcg ggc aaa ttc ttc cgt	240
Leu Ala Asn Thr Pro Phe Ile Val Thr Gly Ser Gly Lys Phe Phe Arg	
65 70 75 80	
aac gtc cag ctt gat cct gcg gct aac tta ggc atc gta aaa gtc gac	288
Asn Val Gln Leu Asp Pro Ala Ala Asn Leu Gly Ile Val Lys Val Asp	
85 90 95	
agc gac ggc ggc tac cac att ctt tgg ggg tta acc aac gaa gcc	336
Ser Asp Gly Ala Gly Tyr His Ile Leu Trp Gly Leu Thr Asn Glu Ala	
100 105 110	
gtc ccc act tcc gaa ctt ccg gct cac ttc ctt tcc cac tgc gag cgc	384
Val Pro Thr Ser Glu Leu Pro Ala His Phe Leu Ser His Cys Glu Arg	
115 120 125	
att aaa gcc acc aac ggc aaa gat cgg gtg atc atg cac tgc cac gcc	432
Ile Lys Ala Thr Asn Gly Lys Asp Arg Val Ile Met His Cys His Ala	
130 135 140	
acc aac ctg atc gcc ctc acc tat gta ctt gaa aac gac acc ggc gtc	480
Thr Asn Leu Ile Ala Leu Thr Tyr Val Leu Glu Asn Asp Thr Ala Val	
145 150 155 160	
ttc act cgc caa ctg tgg gaa ggc agc acc gag tgt ctg gtg gta ttc	528
Phe Thr Arg Gln Leu Trp Glu Gly Ser Thr Glu Cys Leu Val Val Phe	

165	170	175	
ccg gat ggc gtt ggc att ttg ccg tgg atg gtg ccc ggc acg gac gaa			576
Pro Asp Gly Val Gly Ile Leu Pro Trp Met Val Pro Gly Thr Asp Glu			
180	185	190	
atc ggc cag gcg acc gca caa gag atg caa aaa cat tcg ctg gtg ttg			624
Ile Gly Gln Ala Thr Ala Gln Glu Met Gln Lys His Ser Leu Val Leu			
195	200	205	
tgg ccc ttc cac ggc gtc ttc ggc agc gga ccg acg ctg gat gaa acc			672
Trp Pro Phe His Gly Val Phe Gly Ser Gly Pro Thr Leu Asp Glu Thr			
210	215	220	
ttc ggt tta atc gac acc gca gaa aaa tca gca caa gta tta gtg aag			720
Phe Gly Leu Ile Asp Thr Ala Glu Lys Ser Ala Gln Val Leu Val Lys			
225	230	235	240
gtt tat tcg atg ggc ggc atg aaa cag acc atc agc cgt gaa gag ttg			768
Val Tyr Ser Met Gly Gly Met Lys Gln Thr Ile Ser Arg Glu Glu Leu			
245	250	255	
ata gcg ctc ggc aag cgt ttc ggc gtt acg cca ctc gcc agt gcg ctg			816
Ile Ala Leu Gly Lys Arg Phe Gly Val Thr Pro Leu Ala Ser Ala Leu			
260	265	270	
gcg ctg taa			825
Ala Leu			

<210> 13
<211> 274
<212> PRT
<213> Escherichia coli

<400> 13			
Met Gln Asn Ile Thr Gln Ser Trp Phe Val Gln Gly Met Ile Lys Ala			
1	5	10	15
Thr Thr Asp Ala Trp Leu Lys Gly Trp Asp Glu Arg Asn Gly Gly Asn			
20	25	30	
Leu Thr Leu Arg Leu Asp Asp Ala Asp Ile Ala Pro Tyr His Asp Asn			
35	40	45	
Phe His Gln Gln Pro Arg Tyr Ile Pro Leu Ser Gln Pro Met Pro Leu			
50	55	60	
Leu Ala Asn Thr Pro Phe Ile Val Thr Gly Ser Gly Lys Phe Phe Arg			
65	70	75	80
Asn Val Gln Leu Asp Pro Ala Ala Asn Leu Gly Ile Val Lys Val Asp			
85	90	95	
Ser Asp Gly Ala Gly Tyr His Ile Leu Trp Gly Leu Thr Asn Glu Ala			
100	105	110	
Val Pro Thr Ser Glu Leu Pro Ala His Phe Leu Ser His Cys Glu Arg			
115	120	125	
Ile Lys Ala Thr Asn Gly Lys Asp Arg Val Ile Met His Cys His Ala			
130	135	140	
Thr Asn Leu Ile Ala Leu Thr Tyr Val Leu Glu Asn Asp Thr Ala Val			
145	150	155	160
Phe Thr Arg Gln Leu Trp Glu Gly Ser Thr Glu Cys Leu Val Val Phe			
165	170	175	
Pro Asp Gly Val Gly Ile Leu Pro Trp Met Val Pro Gly Thr Asp Glu			
180	185	190	
Ile Gly Gln Ala Thr Ala Gln Glu Met Gln Lys His Ser Leu Val Leu			
195	200	205	
Trp Pro Phe His Gly Val Phe Gly Ser Gly Pro Thr Leu Asp Glu Thr			
210	215	220	
Phe Gly Leu Ile Asp Thr Ala Glu Lys Ser Ala Gln Val Leu Val Lys			
225	230	235	240
Val Tyr Ser Met Gly Gly Met Lys Gln Thr Ile Ser Arg Glu Glu Leu			
245	250	255	

Ile Ala Leu Gly Lys Arg Phe Gly Val Thr Pro Leu Ala Ser Ala Leu
 260 265 270
 Ala Leu

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<210> 14
<211> 939
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
<222> (1)..(936)
<223> coding for rhaR (positive regulator for rhaRS operon)

<400> 14
atg gct ttc tgc aat aac gcg aat ctt ctc aac gta ttt gta cgc cat 48
Met Ala Phe Cys Asn Asn Ala Asn Leu Leu Asn Val Phe Val Arg His
1 5 10 15
att gcg aat aat caa ctt cgt tct ctg gcc gag gta gcc acg gtg gcg 96
Ile Ala Asn Asn Gln Leu Arg Ser Leu Ala Glu Val Ala Thr Val Ala
20 25 30
cat cag tta aaa ctt ctc aaa gat gat ttt ttt gcc agc gac cag cag 144
His Gln Leu Lys Leu Leu Lys Asp Asp Phe Phe Ala Ser Asp Gln Gln
35 40 45
gca gtc gct gtg gct gac cgt tat ccg caa gat gtc ttt gct gaa cat 192
Ala Val Ala Val Ala Asp Arg Tyr Pro Gln Asp Val Phe Ala Glu His
50 55 60
aca cat gat ttt tgt gag ctg gtg att gtc tgg cgc ggt aat ggc ctg 240
Thr His Asp Phe Cys Glu Leu Val Ile Val Trp Arg Gly Asn Gly Leu
65 70 75 80
cat gta ctc aac gat cgc cct tat cgc att acc cgt ggc gat ctc ttt 288
His Val Leu Asn Asp Arg Pro Tyr Arg Ile Thr Arg Gly Asp Leu Phe
85 90 95
tac att cat gct gac gat aaa cac tcc tac gct tcc gtt aac gat ctg 336
Tyr Ile His Ala Asp Asp Lys His Ser Tyr Ala Ser Val Asn Asp Leu
100 105 110
gtt ttg cag aat att att tat tgc ccg gag cgt ctg aag ctg aat ctt 384
Val Leu Gln Asn Ile Ile Tyr Cys Pro Glu Arg Leu Lys Leu Asn Leu
115 120 125
gac tgg cag ggg gcg att ccg gga ttt aac gcc agc gca ggg caa cca 432
Asp Trp Gln Gly Ala Ile Pro Gly Phe Asn Ala Ser Ala Gly Gln Pro
130 135 140
cac tgg cgc tta ggt agc atg ggg atg gcg cag gcg cgg cag gtt atc 480
His Trp Arg Leu Gly Ser Met Gly Met Ala Gln Ala Arg Gln Val Ile
145 150 155 160
ggt cag ctt gag cat gaa agt agt cag cat gtg ccg ttt gct aac gaa 528
Gly Gln Leu Glu His Glu Ser Ser Gln His Val Pro Phe Ala Asn Glu
165 170 175
atg gct gag ttg ctg ttc ggg cag ttg gtg atg ttg ctg aat cgc cat 576
Met Ala Glu Leu Leu Phe Gly Gln Leu Val Met Leu Leu Asn Arg His
180 185 190
cgt tac acc agt gat tcg ttg ccg cca aca tcc agc gaa acg ttg ctg 624
Arg Tyr Thr Ser Asp Ser Leu Pro Pro Thr Ser Ser Glu Thr Leu Leu
195 200 205
gat aag ctg att acc cgg ctg gcg gct agc ctg aaa agt ccc ttt gcg 672
Asp Lys Leu Ile Thr Arg Leu Ala Ala Ser Leu Lys Ser Pro Phe Ala
210 215 220
ctg gat aaa ttt tgt gat gag gca tcg tgc agt gag cgc gtt ttg cgt 720
Leu Asp Lys Phe Cys Asp Glu Ala Ser Cys Ser Glu Arg Val Leu Arg
225 230 235 240

cag caa ttt cgc cag cag act gga atg acc atc aat caa tat ctg cga		768
Gln Gln Phe Arg Gln Gln Thr Gly Met Thr Ile Asn Gln Tyr Leu Arg		
245	250	255
cag gtc aga gtg tgt cat gcg caa tat ctt ctc cag cat agc cgc ctg		816
Gln Val Arg Val Cys His Ala Gln Tyr Leu Leu Gln His Ser Arg Leu		
260	265	270
tta atc agt gat att tcg acc gaa tgt ggc ttt gaa gat agt aac tat		864
Leu Ile Ser Asp Ile Ser Thr Glu Cys Gly Phe Glu Asp Ser Asn Tyr		
275	280	285
ttt tcg gtg gtg ttt acc cgg gaa acc ggg atg acg ccc agc cag tgg		912
Phe Ser Val Val Phe Thr Arg Glu Thr Gly Met Thr Pro Ser Gln Trp		
290	295	300
cgt cat ctc aat tcg cag aaa gat taa		939
Arg His Leu Asn Ser Gln Lys Asp		
305	310	

<210> 15
<211> 312
<212> PRT
<213> Escherichia coli

<400> 15			
Met Ala Phe Cys Asn Asn Ala Asn Leu Leu Asn Val Phe Val Arg His			
1	5	10	15
Ile Ala Asn Asn Gln Leu Arg Ser Leu Ala Glu Val Ala Thr Val Ala			
20	25	30	
His Gln Leu Lys Leu Leu Lys Asp Asp Phe Phe Ala Ser Asp Gln Gln			
35	40	45	
Ala Val Ala Val Ala Asp Arg Tyr Pro Gln Asp Val Phe Ala Glu His			
50	55	60	
Thr His Asp Phe Cys Glu Leu Val Ile Val Trp Arg Gly Asn Gly Leu			
65	70	75	80
His Val Leu Asn Asp Arg Pro Tyr Arg Ile Thr Arg Gly Asp Leu Phe			
85	90	95	
Tyr Ile His Ala Asp Asp Lys His Ser Tyr Ala Ser Val Asn Asp Leu			
100	105	110	
Val Leu Gln Asn Ile Ile Tyr Cys Pro Glu Arg Leu Lys Leu Asn Leu			
115	120	125	
Asp Trp Gln Gly Ala Ile Pro Gly Phe Asn Ala Ser Ala Gly Gln Pro			
130	135	140	
His Trp Arg Leu Gly Ser Met Gly Met Ala Gln Ala Arg Gln Val Ile			
145	150	155	160
Gly Gln Leu Glu His Glu Ser Ser Gln His Val Pro Phe Ala Asn Glu			
165	170	175	
Met Ala Glu Leu Leu Phe Gly Gln Leu Val Met Leu Leu Asn Arg His			
180	185	190	
Arg Tyr Thr Ser Asp Ser Leu Pro Pro Thr Ser Ser Glu Thr Leu Leu			
195	200	205	
Asp Lys Leu Ile Thr Arg Leu Ala Ala Ser Leu Lys Ser Pro Phe Ala			
210	215	220	
Leu Asp Lys Phe Cys Asp Glu Ala Ser Cys Ser Glu Arg Val Leu Arg			
225	230	235	240
Gln Gln Phe Arg Gln Gln Thr Gly Met Thr Ile Asn Gln Tyr Leu Arg			
245	250	255	
Gln Val Arg Val Cys His Ala Gln Tyr Leu Leu Gln His Ser Arg Leu			
260	265	270	
Leu Ile Ser Asp Ile Ser Thr Glu Cys Gly Phe Glu Asp Ser Asn Tyr			
275	280	285	
Phe Ser Val Val Phe Thr Arg Glu Thr Gly Met Thr Pro Ser Gln Trp			
290	295	300	

Arg His Leu Asn Ser Gln Lys Asp
305 310

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<210> 16
<211> 837
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(834)
<223> coding for rhaS (positive regulator of rhaBAD operon)
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<400> 16

atg acc gta tta cat agt gtg gat ttt ttt ccg tct ggt aac gcg tcc	48
Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser	
1 5 10 15	
gtg gcg ata gaa ccc cgg ctc ccg cag gcg gat ttt cct gaa cat cat	96
Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His	
20 25 30	
cat gat ttt cat gaa att gtg att gtc gaa cat ggc acg ggt att cat	144
His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His	
35 40 45	
gtg ttt aat ggg cag ccc tat acc atc acc ggt ggc acg gtc tgt ttc	192
Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe	
50 55 60	
gta cgc gat cat gat cg cat ctg tat gaa cat acc gat aat ctg tgt	240
Val Arg Asp His Asp Arg His Leu Tyr Glu His Thr Asp Asn Leu Cys	
65 70 75 80	
ctg acc aat gtg ctg tat cgc tcg ccg gat cga ttt cag ttt ctc gcc	288
Leu Thr Asn Val Leu Tyr Arg Ser Pro Asp Arg Phe Gln Phe Leu Ala	
85 90 95	
ggg ctg aat cag ttg ctg cca caa gag ctg gat ggg cag tat ccg tct	336
Gly Leu Asn Gln Leu Leu Pro Gln Glu Leu Asp Gly Gln Tyr Pro Ser	
100 105 110	
cac tgg cgc gtt aac cac agc gta ttg cag cag gtg cga cag ctg gtt	384
His Trp Arg Val Asn His Ser Val Leu Gln Gln Val Arg Gln Leu Val	
115 120 125	
gca cag atg gaa cag cag gaa ggg gaa aat gat tta ccc tcg acc gcc	432
Ala Gln Met Glu Gln Gln Glu Gly Glu Asn Asp Leu Pro Ser Thr Ala	
130 135 140	
agt cgc gag atc ttg ttt atg caa tta ctg ctc ttg ctg cgt aaa agc	480
Ser Arg Glu Ile Leu Phe Met Gln Leu Leu Leu Leu Arg Lys Ser	
145 150 155 160	
agt ttg cag gag aac ctg gaa aac agc gca tca cgt ctc aac ttg ctt	528
Ser Leu Gln Glu Asn Leu Glu Asn Ser Ala Ser Arg Leu Asn Leu Leu	
165 170 175	
ctg gcc tgg ctg gag gac cat ttt gcc gat gag gtg aat tgg gat gcc	576
Leu Ala Trp Leu Glu Asp His Phe Ala Asp Glu Val Asn Trp Asp Ala	
180 185 190	
gtg gcg gat caa ttt tct ctt tca ctg cgt acg cta cat cgg cag ctt	624
Val Ala Asp Gln Phe Ser Leu Ser Leu Arg Thr Leu His Arg Gln Leu	
195 200 205	
aag cag caa acg gga ctg acg cct cag cga tac ctg aac cgc ctg cga	672
Lys Gln Gln Thr Gly Leu Thr Pro Gln Arg Tyr Leu Asn Arg Leu Arg	
210 215 220	
ctg atg aaa gcc cga cat ctg cta cgc cac acg gag gcc agc gtt act	720
Leu Met Lys Ala Arg His Leu Leu Arg His Ser Glu Ala Ser Val Thr	
225 230 235 240	
gac atc gcc tat cgc tgt gga ttc acg gac agt aac cac ttt tcg acg	768

Asp Ile Ala Tyr Arg Cys Gly Phe Ser Asp Ser Asn His Phe Ser Thr
 245 250 255
 ctt ttt cgc cga gag ttt aac tgg tca ccg cgt gat att cgc cag gga 816
 Leu Phe Arg Arg Glu Phe Asn Trp Ser Pro Arg Asp Ile Arg Gln Gly
 260 265 270
 cgg gat ggc ttt ctg caa taa
 Arg Asp Gly Phe Leu Gln
 275

<210> 17
 <211> 278
 <212> PRT
 <213> Escherichia coli

<400> 17
 Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser
 1 5 10 15
 Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His
 20 25 30
 His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His
 35 40 45
 Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe
 50 55 60
 Val Arg Asp His Asp Arg His Leu Tyr Glu His Thr Asp Asn Leu Cys
 65 70 75 80
 Leu Thr Asn Val Leu Tyr Arg Ser Pro Asp Arg Phe Gln Phe Leu Ala
 85 90 95
 Gly Leu Asn Gln Leu Leu Pro Gln Glu Leu Asp Gly Gln Tyr Pro Ser
 100 105 110
 His Trp Arg Val Asn His Ser Val Leu Gln Gln Val Arg Gln Leu Val
 115 120 125
 Ala Gln Met Glu Gln Gln Glu Gly Glu Asn Asp Leu Pro Ser Thr Ala
 130 135 140
 Ser Arg Glu Ile Leu Phe Met Gln Leu Leu Leu Leu Arg Lys Ser
 145 150 155 160
 Ser Leu Gln Glu Asn Leu Glu Asn Ser Ala Ser Arg Leu Asn Leu Leu
 165 170 175
 Leu Ala Trp Leu Glu Asp His Phe Ala Asp Glu Val Asn Trp Asp Ala
 180 185 190
 Val Ala Asp Gln Phe Ser Leu Ser Leu Arg Thr Leu His Arg Gln Leu
 195 200 205
 Lys Gln Gln Thr Gly Leu Thr Pro Gln Arg Tyr Leu Asn Arg Leu Arg
 210 215 220
 Leu Met Lys Ala Arg His Leu Leu Arg His Ser Glu Ala Ser Val Thr
 225 230 235 240
 Asp Ile Ala Tyr Arg Cys Gly Phe Ser Asp Ser Asn His Phe Ser Thr
 245 250 255
 Leu Phe Arg Arg Glu Phe Asn Trp Ser Pro Arg Asp Ile Arg Gln Gly
 260 265 270
 Arg Asp Gly Phe Leu Gln
 275

<210> 18
 <211> 1035
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS

<222> (1)..(1032)
<223> coding for rhaT (rhamnose transport protein)

<400> 18
atg agt aac gcg att acg atg ggg ata ttt tgg cat ttg atc ggc gcg 48
Met Ser Asn Ala Ile Thr Met Gly Ile Phe Trp His Leu Ile Gly Ala
1 5 10 15
gcc agt gca gcc tgt ttt tac gct ccg ttc aaa aaa gta aaa aaa tgg 96
Ala Ser Ala Ala Cys Phe Tyr Ala Pro Phe Lys Lys Val Lys Lys Trp
20 25 30
tca tgg gaa acc atg tgg tca gtc ggt ggg att gtt tcg tgg att att 144
Ser Trp Glu Thr Met Trp Ser Val Gly Gly Ile Val Ser Trp Ile Ile
35 40 45
ctg ccg tgg gcc atc agc gcc ctg tta cta ccg aat ttc tgg gcg tat 192
Leu Pro Trp Ala Ile Ser Ala Leu Leu Pro Asn Phe Trp Ala Tyr
50 55 60
tac agc tcg ttt agt ctc tct acg cga ctg cct gtt ttt ctg ttc ggc 240
Tyr Ser Ser Phe Ser Leu Ser Thr Arg Leu Pro Val Phe Leu Phe Gly
65 70 75 80
gct atg tgg ggg atc ggt aat atc aac tac ggc ctg acc atg cgt tat 288
Ala Met Trp Gly Ile Gly Asn Ile Asn Tyr Gly Leu Thr Met Arg Tyr
85 90 95
ctc ggc atg tcg atg gga att ggc atc gcc att ggc att acg ttg att 336
Leu Gly Met Ser Met Gly Ile Gly Ile Ala Ile Gly Ile Thr Leu Ile
100 105 110
gtc ggt acg ctg atg acg cca att atc aac ggc aat ttc gat gtg ttg 384
Val Gly Thr Leu Met Thr Pro Ile Ile Asn Gly Asn Phe Asp Val Leu
115 120 125
att agc acc gaa ggc gga cgc atg acg ttg ctc ggc gtt ctg gtg gcg 432
Ile Ser Thr Glu Gly Arg Met Thr Leu Leu Gly Val Leu Val Ala
130 135 140
ctg att ggc gta ggg att gta act cgc gcc ggg cag ttg aaa gag cgc 480
Leu Ile Gly Val Gly Ile Val Thr Arg Ala Gly Gln Leu Lys Glu Arg
145 150 155 160
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Lys Met Gly Ile Lys Ala Glu Glu Phe Asn Leu Lys Lys Gly Leu Val
165 170 175
ctg gcg gtg atg tgc ggc att ttc tct gcc ggg atg tcc ttt gcg atg 576
Leu Ala Val Met Cys Gly Ile Phe Ser Ala Gly Met Ser Phe Ala Met
180 185 190
aac gcc gca aaa ccg atg cat gaa gcc gct gcc gca ctt ggc gtc gat 624
Asn Ala Ala Lys Pro Met His Glu Ala Ala Ala Leu Gly Val Asp
195 200 205
cca ctg tat gtc gct ctg cca agc tat gtt gtc atc atg ggc ggc ggc 672
Pro Leu Tyr Val Ala Leu Pro Ser Tyr Val Val Ile Met Gly Gly Gly
210 215 220
gcg atc att aac ctc ggt ttc tgt ttt att cgt ctg gca aaa gtg aag 720
Ala Ile Ile Asn Leu Gly Phe Cys Phe Ile Arg Leu Ala Lys Val Lys
225 230 235 240
gat ttg tcg cta aaa gcc gac ttc tcg ctg gca aaa tcg ctg atc att 768
Asp Leu Ser Leu Lys Ala Asp Phe Ser Leu Ala Lys Ser Leu Ile Ile
245 250 255
cac aat gtg tta ctc tcg aca ctg ggc ggg ttg atg tgg tat ctg caa 816
His Asn Val Leu Leu Ser Thr Leu Gly Gly Leu Met Trp Tyr Leu Gln
260 265 270
ttc ttt ttc tat gcc tgg ggc cac gcc cgc att ccg gcg cag tat gac 864
Phe Phe Phe Tyr Ala Trp Gly His Ala Arg Ile Pro Ala Gln Tyr Asp
275 280 285
tac atc agt tgg atg ctg cat atg agt ttc tat gta ttg tgc ggc ggt 912
Tyr Ile Ser Trp Met Leu His Met Ser Phe Tyr Val Leu Cys Gly Gly
290 295 300

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305 310 315 320	
gta acg gtg ttg agc ctc ggt tgt gtg att att gtc gcc gct aac Val Thr Val Leu Ser Leu Gly Cys Val Val Ile Ile Val Ala Ala Asn	1008
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Ser Trp Glu Thr Met Trp Ser Val Gly Gly Ile Val Ser Trp Ile Ile	
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Leu Pro Trp Ala Ile Ser Ala Leu Leu Leu Pro Asn Phe Trp Ala Tyr	
50 55 60	
Tyr Ser Ser Phe Ser Leu Ser Thr Arg Leu Pro Val Phe Leu Phe Gly	
65 70 75 80	
Ala Met Trp Gly Ile Gly Asn Ile Asn Tyr Gly Leu Thr Met Arg Tyr	
85 90 95	
Leu Gly Met Ser Met Gly Ile Gly Ile Ala Ile Gly Ile Thr Leu Ile	
100 105 110	
Val Gly Thr Leu Met Thr Pro Ile Ile Asn Gly Asn Phe Asp Val Leu	
115 120 125	
Ile Ser Thr Glu Gly Gly Arg Met Thr Leu Leu Gly Val Leu Val Ala	
130 135 140	
Leu Ile Gly Val Gly Ile Val Thr Arg Ala Gly Gln Leu Lys Glu Arg	
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